

Figure 1  
VAKTI-1 cDNA and its translation into  
amino acid sequence

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Frame 2

ATG CAT GGA GTG GAC CTG TAG GCG ACT TGC ATC GTC TTC AAC ATG AAG ATA GCC	M K I A				
10 19 28 37 46 55					
————MEMC-1————  T V S V L L P L A L C L I Q D A A S  K N ACA GTG TCA GTG CTT CTG CCC TTG GCT CTT TGC CTC ATA CAA GAT GCT GCC ACT AAG AAT					
64 73 82 91 100 109	————>HF6479————				
E D Q E M C H E F Q A F M K N G K L F C GAA GAT CAG GAA ATG TGC CAT GAA TTT CAG GCA TTT ATG AAA AAT GGA AAA CTG TTC TGT					
124 133 142 151 160 169					
←————CHEF-14————  P Q D K K F F Q S L D G I M F I N K C A CCC CAG GAT AAG AAA TTT TTT CAA ACT CTT GAT GGA ATA ATG TTC ATC AAT AAA TGT GCC					
184 193 202 211 220 229	←————CHEF-2————				
←————CHEF-2————  HF6479 ←————  T C K M I L E K E A K S Q I K R A R H L A ACG TGC AAA ATG ATA CTG GAA AAA GCA AAA TCA CAG AAG AGG GCC AGG CAT TTA GCA					
244 253 262 271 280 289					
R A P K A T A P T E L N C D D F K K G E AGA GCT CCC AAG GCT ACT GCC CCA ACA GAG CTG AAT TGT GAT GAT TTT AAA AAA GGA GAA					
304 313 322 331 340 349					
R D G D F I C P D Y Y E A V C G T D G K AGA GAT GGG GAT TTT ATC TGT CCT GAT TAT TAT GAA GCT GTT TGT GGC ACA GAT GGG AAA					
364 373 382 391 400 409					
T Y D N R C A L C A E N A K T G S Q I G ACA TAT GAC AAC AGA TGT GCA CTG TGT GCT GAG AAT GCG AAA ACC GGG TCC CAA ATT GGT					
424 433 442 451 460 469					
V K S E G E C K S S N P E Q V R S I V S GTA AAA AGT GAA GGG GAA TGT AAG AGC ACT AAT CCA GAG CAG GTG AGG TCA ATT GTC AGC					
484 493 502 511 520 529					
L M G N T G R L T S N S K STOP CTG ATG GCA AAT ACT GGG AGG CTA ACT TCA AAT AGT AAG TAG GTG CTG TCC TCT TCC TTC					
544 553 562 571 580 589					
TTA GGT GGG AGC CTT GGA AGG AAT TAA TTC TTG CTT TAT GTG AAA TGG AAT ACC CAG TTA					
604 613 622 631 640 649					
CTG CCC ACT AAT ATG AAA AAG CTA ATT ATA GTC TCT GAA ACT GGA TCA GAT TAC TTT GGT					
664 673 682 691 700 709					
GGT TAA GAT CTT TCA ATC TAT TGC TGC TTT GTA T					
724 733 742 749					

Figure 2  
VAKTI-2 cDNA and its translation into  
amino acid sequence

Frame 2

ATG	CAT	GGA	GTG	GAC	CTG	TAG	GCG	ACT	TGC	ATC	GTC	TTC	AAC	ATG	AAG	ATA	GCC
10														M	K	I	A
														37	46	55	

T	V	S	V	L	L	P	L	A	L	C	L	I	Q	D	A	A	S	--> HF 6479	
ACA	GTG	TCA	GTG	CTT	CTG	CCC	TTG	GCT	CTT	TGC	CTC	ATA	CAA	GAT	GCT	GCC	AGT	AAG	AAT
64		73		82									91		100		109		

Repeat 1

E	D	Q	E	M	C	H	E	F	Q	A	F	M	K	N	G	K	L	F	C
GAA	GAT	CAG	GAA	ATG	TGC	CAT	GAA	TTT	CAG	GCA	TTT	ATG	AAA	AAT	GGA	AAA	CTG	TTC	TGT
124		133		142								151		160		169			

P	Q	D	K	K	F	F	Q	S	L	D	G	I	M	F	I	N	K	C	#
CCC	CAG	GAT	AAG	AAA	TTT	TTT	CAA	AGT	CTT	GAT	GGA	ATA	ATG	TTC	ATC	ATAT	AAA	TGT	GCC
184		193		202								211		220		229			

T	C	K	M	I	L	E	K	E	A	K	S	Q	I	K	R	A	R	H	L	A
ACG	TGC	AAA	ATG	ATA	CTG	GAA	AAA	GAA	GCA	AAA	TCA	CAG	AAG	AGG	GCC	AGG	CAT	TTA	GCA	
244		253		262								271		280		289				

typical Kazal domain

R	A	P	K	A	T	A	P	T	E	L	N	C	D	D	F	K	K	G	E
AGA	GCT	CCC	AAG	GCT	ACT	GCC	CCA	ACA	GAG	CTG	AAAT	TGT	GAT	GAT	TTT	AAA	AAA	GGA	GAA
304		313		322								331		340		349			

R	D	G	D	F	I	C	P	D	Y	Y	E	A	V	C	G	T	D	G	K
AGA	GAT	GGG	GAT	TTT	ATC	TGT	CCT	GAT	TAT	TAT	GAA	GCT	GTT	TGT	GGC	ACA	GAT	GGG	AAA
364		373		382							391		400		409				

T	Y	D	N	R	C	A	L	C	A	E	N	A	K	T	G	S	Q	I	G
ACA	TAT	GAC	AAC	AGA	TGT	GCA	CTG	TGT	GCT	GAG	AAT	GCG	AAA	ACC	GGG	TCC	CAA	ATT	GGT
424		433		442							451		460		469				

Repeat 2

V	K	S	E	G	E	C	K	S	S	N	P	E	Q	D	V	C	S	A	F
GTA	AAA	AGT	GAA	GGG	GAA	TGT	AAG	AGC	AGT	AAT	CCA	GAG	CAG	GAT	GTA	TGC	AGT	GCT	TTT
484		493		502							511		520		529				

R	P	F	V	R	N	G	R	L	G	C	T	R	E	N	D	P	V	L	G
CGG	CCC	TTT	GTT	AGA	AAT	GGA	AGA	CTT	GGA	TGC	ACA	AGG	GAA	AAT	GAT	CCT	GTT	CTT	GGT
544		553		562							571		580		589				

P	D	G	K	T	H	G	N	K	C	A	M	C	A	E	L	F	L	K	E
CCT	GAT	GGG	AAG	ACG	CAT	GGC	AAT	AAG	TGT	GCA	ATG	TGT	GCT	GAG	CTG	TTT	TTA	AAA	GAA
604		613		622							631		640		649				

A	E	N	A	K	R	E	G	E	T	R	I	R	R	N	A	E	K	D	F
GCT	GAA	AAT	GCC	AAG	CGA	GAG	GGT	GAA	ACT	AGA	ATT	CGA	CGA	AAT	GCT	GAA	AAG	GAT	TTT
664		673		682							691		700		709				

Repeat 3

C	K	E	Y	E	K	Q	V	R	N	G	R	L	F	C	T	R	E	S	D
TGC	AAG	GAA	TAT	GAA	AAA	CAA	GTG	AGA	AAT	GGA	AGG	CTT	TTT	TGT	ACA	CGG	GAG	AGT	GAT
724		733		742							751		760		769				

P	V	R	G	P	D	G	R	M	H	G	N	K	C	A	L	C	A	E	I
CCA	GTC	CGT	GGC	CCT	GAC	GGC	AGG	ATG	CAT	GGC	AAC	AAA	TGT	GCC	CTG	TGT	GCT	GAA	ATT
784		793		802							811		820		829				

F	K	R	R	F	S	E	E	N	S	K	T	D	Q	N	L	G	K	A	E
TTC	AAG	CGG	CGT	TTT	TCA	GAG	GAA	AAC	AGT	AAA	ACA	GAT	CAA	AAT	TTG	GGA	AAA	GCT	GAA
844		853		862							871		880		889				

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## Repeat 4

E	K	T	K	V	K	R	E	I	V	K	L	C	S	Q	Y	Q	N	Q	A
GAA	AAA	ACT	AAA	GTT	AAA	AGA	GAA	ATT	GTG	AAA	CTC	TGC	AGT	CAA	TAT	CAA	AAT	CAG	GCA
904				913				922			931			940			949		

K	N	G	I	L	F	C	T	R	E	N	D	P	I	R	G	P	D	G	K
AAG	AAT	GGA	ATA	CTT	TTC	TGT	ACC	AGA	GAA	AAT	GAC	CCT	ATT	CGT	GGT	CCA	GAT	GGG	AAA
964		973				982			991			1000			1009				

M	H	G	N	L	C	S	M	C	Q	V	Y	F	Q	A	E	N	E	E	K
ATG	CAT	GGC	AAC	TTG	TGT	TCC	ATG	TGT	CAA	GTC	TAC	TTC	CAA	GCA	GAA	AAT	GAA	GAA	AAG
1024		1033				1042			1051			1060			1069				

| → HF 7665

K	K	A	E	A	R	A	R	N	K	R	E	S	G	K	A	T	S	Y	A
AAA	AAG	GCT	GAA	GCA	CGA	GCT	AGA	AAC	AAA	AGA	GAA	TCT	GGG	AAA	GCA	ACC	TCA	TAT	GCA
1084		1093				1102			1111			1120			1129				

## Repeat 5

E	L	C	N	E	Y	R	K	L	V	R	N	G	K	L	A	C	T	R	E
GAG	CTT	TGC	AAT	GAA	TAT	CGA	AAG	CTT	GTG	AGG	AAC	GGG	AAA	CTT	GCT	TGC	ACC	AGA	GAG
1144		1153				1162			1171			1180			1189				

N	D	P	I	Q	G	P	D	G	K	V	H	G	N	T	C	S	M	C	E
AAC	GAT	CCT	ATT	CAG	GGC	CCA	GAT	GGG	AAA	GTG	CAC	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAG
1204		1213			1222			1231			1240			1249					

HF 7665 ← |

V	F	F	Q	A	E	E	E	E	K	K	K	K	E	G	E	S	R	N	K
GTT	TTT	TTC	CAA	GCA	GAA	GAA	GAA	GAA	AAG	AAA	AAG	AAG	GAA	GGC	GAA	TCA	AGA	AAC	AAA
1264		1273			1282			1291			1300			1309					

## Repeat 6

R	Q	S	K	S	T	A	S	F	E	E	L	C	S	E	Y	R	K	S	R
AGA	CAA	TCT	AAG	AGT	ACA	GCT	TCC	TTT	GAG	GAG	TTG	TGT	AGT	GAA	TAC	CGC	AAA	TCC	AGG
1324		1333				1342			1351			1360			1369				

K	N	G	R	L	F	C	T	R	E	N	D	P	I	Q	G	P	D	G	K
AAA	AAC	GGA	CGG	CTT	TTT	TGC	ACC	AGA	GAG	AAT	GAC	CCC	ATC	CAG	GGC	CCA	GAT	GGG	AAA
1384		1393			1402			1411			1420			1429					

M	H	G	N	T	C	S	M	C	E	A	F	F	Q	Q	E	E	R	A	R
ATG	CAT	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAG	GCC	TTC	TTT	CAA	CAA	GAA	GAA	AGA	GCA	GAG
1444		1453			1462			1471			1480			1489					

## Repeat 7

A	K	A	K	R	E	A	A	K	E	I	C	S	E	F	R	D	Q	V	R
GCA	AAG	GCT	AAA	AGA	GAA	GCT	GCA	AAG	GAA	ATC	TGC	AGT	GAA	TTT	CGG	GAC	CAA	GTG	AGG
1504		1513			1522			1531			1540			1549					

N	G	T	L	I	C	T	R	E	H	N	P	V	R	G	P	D	G	K	M
AAT	GGA	ACA	CTT	ATA	TGC	ACC	AGG	GAG	CAT	AAT	CCT	GTC	CGT	GGA	CCA	GAT	GGC	AAA	ATG
1564		1573			1582			1591			1600			1609					

H	G	N	K	C	A	M	C	À	S	V	F	K	L	E	E	E	K	K	
CAT	GGA	AAC	AAG	TGT	GCC	AGT	GCC	AGT	GTC	AAA	CTT	GAA	GAA	GAA	GAG	AAG	AAA		
1624		1633			1642			1651			1660			1669					

N	D	K	E	E	K	G	K	V	E	A	E	K	V	K	R	E	A	V	Q
AAT	GAT	AAA	GAA	GAA	AAA	GGG	AAA	GTT	GAG	GCT	GAA	AAA	GTT	AAG	AGA	GAA	GCA	GTT	CAG
1684		1693			1702			1711			1720			1729					

## Repeat 8

E	L	C	S	E	Y	R	H	Y	V	R	N	G	R	L	P	C	T	R	E
GAG	CTG	TGC	AGT	GAA	TAT	CGT	CAT	TAT	GTG	AGG	AAT	GGG	CGA	CTC	CCC	TGT	ACC	AGA	GAG
1744		1753			1762			1771			1780			1789					

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N	D	P	I	E	G	L	D	G	K	I	H	G	N	T	C	S	M	C	E	
AAT	GAT	CCT	ATT	GAG	GGT	CTA	GAT	GGG	AAA	ATC	CAC	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAA	
1804		1813		1822		1831				1840		1849								

A	F	F	Q	Q	E	A	K	E	K	E	R	A	E	P	R	A	K	V	K
GCC	TTC	TTC	CAG	CAA	GAA	GCA	AAA	GAA	AAA	GAA	AGA	GCT	GAA	CCC	AGA	GCA	AAA	GTC	AAA
1864		1873		1882		1891		1891		1900		1909							

Repeat 9

R	E	A	E	K	E	T	C	D	E	F	R	R	L	L	Q	N	G	K	L
AGA	GAA	GCT	GAA	AAG	GAG	ACA	TGC	GAT	GAA	TTT	CGG	AGA	CTT	TTG	CAA	AAT	GGA	AAA	CTT
1924		1933		1942		1951		1951		1960		1969							

F	C	T	R	E	N	D	P	V	R	G	P	O	G	K	T	H	G	N	K
TTC	TGC	ACA	AGA	GAA	AAT	GAT	CCT	GTG	CGT	GGC	CCA	GAT	GGC	AAG	ACC	CAT	GCG	AAC	AAG
1984		1993		2002		2011		2011		2020		2029							

#

C	A	M	C	K	A	V	F	Q	K	E	N	E	E	R	K	R	K	E	E
TGT	GCC	ATG	TGT	AAG	GCA	GTC	TTC	CGA	AAA	GAA	AAT	GAG	GAA	AGA	AAG	AGG	AAA	GAA	GAG
2044		2053		2062		2071		2071		2080		2089							

E	D	Q	R	N	A	A	G	H	G	S	S	G	G	G	G	G	N	T	Q
GAA	GAT	CAG	AGA	AAT	GCT	GCA	GGA	CAT	GGT	TCC	AGT	GGT	GGT	GGA	GGA	GGA	AAC	ACT	CAG
2104		2113		2122		2131		2131		2140		2149							

Repeat 10

D	E	C	A	E	Y	R	E	Q	M	K	N	G	R	L	S	C	T	R	E
GAC	GAA	TGT	GCT	GAG	TAT	CGG	GAA	CAA	ATG	AAA	AAT	GGA	AGA	CTC	AGC	TGT	ACT	CGG	GAG
2164		2173		2182		2191		2191		2200		2209							

S	D	P	V	R	D	A	D	G	K	S	Y	N	N	Q	C	T	M	C	K
AGT	GAT	CCT	GTA	CGT	GAT	GCT	GAT	GGC	AAA	TCG	TAC	AAC	AAT	CAG	TGT	ACC	ATG	TGT	AAA
2224		2233		2242		2251		2251		2260		2269							

A	K	L	E	R	E	A	E	R	K	N	E	Y	S	R	S	R	S	N	G
GCA	AAA	TTG	GAA	AGA	GAA	GCA	GAG	AGA	AAA	AAT	GAG	TAT	TCT	CGC	TCC	AGA	TCA	AAT	GGG
2284		2293		2302		2311		2311		2320		2329							

Repeat 11

T	G	S	E	S	G	K	D	T	C	D	E	F	R	S	Q	M	K	N	G
ACT	GGA	TCA	GAA	TCA	GGG	AAG	GAT	ACA	TGT	GAT	GAG	TTT	AGA	AGC	CAA	ATG	AAA	AAT	GGA
2344		2353		2362		2371		2371		2380		2389							

K	L	I	C	T	R	E	S	D	P	V	R	G	P	D	G	K	T	H	G
AAA	CTT	ATC	TGC	ACT	CGA	GAA	AGT	GAC	CCT	GTC	CGG	GGT	CCA	GAT	GGC	AAG	ACA	CAT	GGT
2404		2413		2422		2431		2431		2440		2449							

N	K	C	T	M	C	K	E	K	L	E	R	E	A	A	E	K	K	R	K
ATAT	AAG	TGT	ACT	ATG	TGT	AAG	GAA	AAA	CTG	GAA	AGG	GAA	GCA	GCT	GAA	AAA	AAA	AGA	AAG
2464		2473		2482		2491		2491		2500		2509							

R	M	K	T	G	A	I	Q	E	K	G	A	I	Q	E	K	G	A	M	T
AGG	ATG	AAG	ACA	GGG	GCA	ATA	CAG	GAG	AAA	GGA	GCA	ATA	CAG	GAG	AAA	GGA	GCA	ATG	ACA
2524		2533		2542		2551		2551		2560		2569							

K	R	I	C	V	V	N	F	E	A	C	R	E	M	E	S	L	S	A	P
AAG	AGG	ATC	TGT	GTC	GTG	AAT	TTC	GAA	GCA	TGC	AGA	GAA	ATG	GAA	AGC	TTA	TCT	GCA	CCA
2584		2593		2602		2611		2611		2620		2629							

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E K I T L F E A H M A R C T S I N V L C  
 GAG AAA ATA ACC CTG TTC GAG GCC CAT ATG GCA AGA TGC ACA TCA ATA AAT GTG CTA TGT  
 2644 2653 2662 2671 2680 2689

V R A S L I E K L M K E K R K M K R N Q  
 GTC AGA GCA TCT TTG ATC GAG AAG CTA ATG AAA GAA AAA AGA AAG ATG AAG AGA AAT CAA  
 2704 2713 2722 2731 2740 2749

V A S P Q I M Q R M S A V N F E T I STOP  
 GTA GCA AGC CCT CAA ATA ATG CAA AGG ATG AGT GCA GTG AAT TTC GAA ACT ATA TAA GGA  
 2764 2773 2782 2791 2800 2809

ACA ATG AAC TCA TCT GCC CTA GAG AGA ATG ACC CAG TGC ACG GTG CTG ATG GAA AGT TCT  
 2824 2833 2842 2851 2860 2869

ATA CAA ACA AGT GCT ACA TGT GCA GAG CTG TCT TTC TAA CAG AAG CTT TGG AAA GGG CAA  
 2884 2893 2902 2911 2920 2929

AGC TTC AAG AAA AAC CAT CCC ATG TTA GAG CTT CTC AAG AGG AAG ACA GCC CAG ACT CTT  
 2944 2953 2962 2971 2980 2989

TCA GTT CTC TGG ATT CTG AGA TGT GCA AAG ACT ACC GAG TAT TGC CCA GGA TAG GCT ATC  
 3004 3013 3022 3031 3040 3049

TTT GTC CAA AGG ATT TAA AGC CTG TCT GTG GTG AGC ATG GCC AAA CCT ACA ACA ATC CTT  
 3064 3073 3082 3091 3100 3109

GCA TGC TCT GTC ATG AAA ACC TGA TAC GCC AAA CAA ATA CAC ACA TCC GCA GTA CAG GGA  
 3124 3133 3142 3151 3160 3169

AGT GTG AGG AGA GCA GCA CCC CAG GAA CCA CCG CAG CCA GCA TGC CCC CGT TTG ACG AAT  
 3184 3193 3202 3211 3220 3229

GAC AGG AAG ATT GTT GAA AGC CAT GAG GGA AAA AAT AAA CCC CAG TTT TGA ATC ACC TAC  
 3244 3253 3262 3271 3280 3289

CTT CAC CAT CTG TAT ATA CAA AGA ATT TTT CGG AGC TTG TTT TAT TTG CTA TAG AAA ACA  
 3304 3313 3322 3331 3340 3349

ATA CAG AGC TTT TGG GAA TGG AAT CAC TGA TTT TCA GTC TTT TCC ATT TCT TTC CTC CTA  
 3364 3373 3382 3391 3400 3409

GAA TCT GTG ATC TGA GGG TAT AAA GAC ATT TCC ACC AAG TTT GAG CCC TCA AAA TGT CCT  
 3424 3433 3442 3451 3460 3469

#### polyadenylation signal

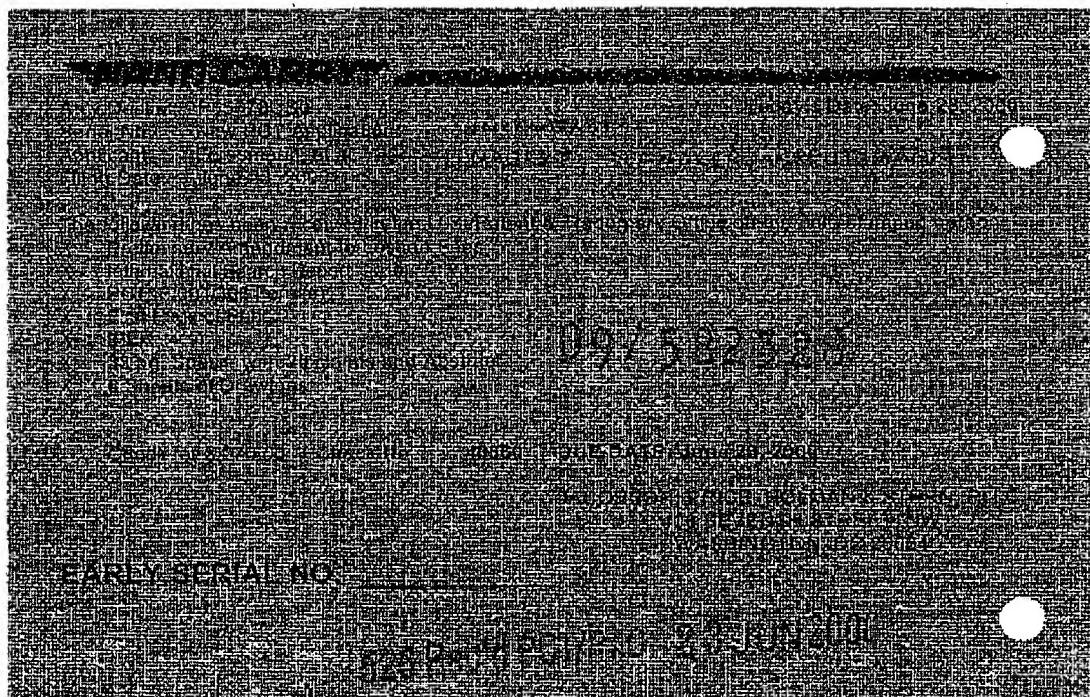
GAT TAC ATA GCT GTC TGT CCA ACT GCC TGT TCA ATA AAA GTA AAC TCA GCA GAA AAA....  
 3484 3493 3502 3511 3520 3529

.....poly(A) tail

MAY. 3. 2005 3:15PM

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